

SEQUENCE LISTING

<110> Freyssinet, Georges
Rang, Cecile
Frutos, Roger

<120> Pepsin-sensitive modified *Bacillus thuringiensis* insecticidal toxin

<130> A35992-PCT-USA-A (072667.0191)

<140> To Be Assigned

<141> September 19, 2003

<150> PCT/FR02/00772

<151> March 4, 2002

<150> FR 01/03691

<151> March 19, 2001

<160> 160

<170> PatentIn Ver. 2.1

<210> 1

<211> 2019

<212> DNA

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<220>

<221> CDS

<222> (1)..(2019)

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Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile	
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Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg	
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Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	
	530					535					540					
cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	gtt	aat	1680
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	
545					550					555					560	
tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	gtt	cgt	ttt	gcc	tca	aca	1728
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr	
				565				570						575		
gga	aat	ttc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	ggt	gat	1776
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp	
			580					585					590			
gtt	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	tac	gaa	1824
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu	
		595					600					605				
tcc	ttt	ttc	aca	aga	gag	ttt	act	act	act	ggt	ccg	ttc	aat	ccg	cct	1872
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro	
	610					615					620					
ttt	aca	ttt	aca	caa	gct	caa	gag	att	cta	aca	gtg	aat	gca	gaa	ggt	1920

Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly	
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gtt	agc	acc	ggt	ggt	gaa	tat	tat	ata	gat	aga	att	gaa	att	gtc	cct	1968
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro	
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gtg	aat	ccg	gca	cga	gaa	gcg	gaa	gag	gat	tta	gaa	gcg	gcg	aag	aaa	2016
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys	
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gcg																2019
Ala																

<210> 4
 <211> 673
 <212> PRT
 <213> Artificial sequence
 <223> Artificial sequence description: Cry9Ca1 Leu-164

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Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
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Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
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Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
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Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
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Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
			100					105					110			
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
	115						120					125				
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
	130					135					140					
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
145					150					155				160		
Asn	Asp	Thr	Leu	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
			165						170					175		
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
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Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu			
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Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr			
	210					215					220							
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala			
225					230					235					240			
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg			
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Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg			
			260					265					270					
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr			
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Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg			
	290					295					300							
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly			
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Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu			
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Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala			
	370					375					380							
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile			
385					390					395					400			
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp			
				405					410					415				
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe			
			420					425					430					
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly			
		435					440					445						
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser			
	450					455					460							
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe			
465					470					475					480			
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr			
				485					490					495				

Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro
			500					505					510		
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser
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Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu
	530					535					540				
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn
545					550					555					560
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr
				565					570					575	
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp
			580					585					590		
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu
		595					600					605			
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro
	610					615					620				
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly
625					630					635					640
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro
				645					650					655	
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys
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 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
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Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
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cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
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aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
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Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
	65				70					75					80	
ctc	ggg	gct	tta	ggt	ggt	ccg	ttt	tct	gga	caa	ata	gtg	agt	ttt	tat	288
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
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caa	ttc	ctt	tta	aat	aca	ctg	tgg	cca	ggt	aat	gat	aca	gct	ata	tgg	336
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
			100					105					110			
gaa	gct	ttc	atg	cga	cag	gtg	gag	gaa	ctt	gtc	aat	caa	caa	ata	aca	384
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
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gaa	ttt	gca	aga	aat	cag	gca	ctt	gca	aga	ttg	caa	gga	tta	gga	gac	432
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp	
	130					135					140					
tct	ttt	aat	gta	tat	caa	cgt	tcc	ctt	caa	aat	tgg	ttg	gct	gat	cga	480
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
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aat	gat	aca	ttt	aat	tta	agt	ggt	ggt	cgt	gct	caa	ttt	ata	gct	tta	528
Asn	Asp	Thr	Phe	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
gac	ctt	gat	ttt	ggt	aat	gct	att	cca	ttg	ttt	gca	gta	aat	gga	cag	576
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
			180					185					190			
cag	ggt	cca	tta	ctg	tca	gta	tat	gca	caa	gct	gtg	aat	tta	cat	ttg	624
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu	
		195					200					205				
tta	tta	tta	aaa	gat	gca	tct	ctt	ttt	gga	gaa	gga	tgg	gga	ttc	aca	672
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
	210					215					220					
cag	ggg	gaa	att	tcc	aca	tat	tat	gac	cgt	caa	ttg	gaa	cta	acc	gct	720
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
	225				230					235					240	
aag	tac	act	aat	tac	tgt	gaa	act	tgg	tat	aat	aca	ggt	tta	gat	cgt	768
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg	

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Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg	
			260					265					270			
aga	gaa	atg	act	tta	gtg	gta	tta	gat	gtt	gtg	gcg	cta	ttt	cca	tat	864
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr	
		275					280					285				
tat	gat	gta	cga	ctt	tat	cca	acg	gga	tca	aac	cca	cag	ctt	aca	cgt	912
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	
	290					295					300					
gag	gta	tat	aca	gat	ccg	att	gta	ttt	aat	cca	cca	gct	aat	gtt	gga	960
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly	
305					310					315					320	
ctt	tgc	cga	cgt	tgg	ggg	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325					330					335		
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	
			340					345					350			
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gat	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	
		355					360					365				
tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
	370					375					380					
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
385					390					395					400	
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
				405				410						415		
ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
			420				425						430			
gtc	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	gga	gga	1344
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
		435					440					445				
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
	450					455					460					
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	agc	ttt	1440
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	
465					470					475					480	

caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	
485 490 495	
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca	1536
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	
515 520 525	
ggt act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat	1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn	
545 550 555 560	
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca	1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr	
565 570 575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat	1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp	
580 585 590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa	1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	
595 600 605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt	1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly	
625 630 635 640	
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct	1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro	
645 650 655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa	2016
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660 665 670	
gcg	2019
Ala	

<210> 6

<211> 673

<212> PRT

<213> Artificial sequence

<223> Artificial sequence description: Cry9Ca1 Phe-164

<400> 6

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			20					25					30		
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met
		35					40					45			
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile
	50					55					60				
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile
65					70					75					80
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr
				85					90					95	
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp
			100					105					110		
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr
		115					120					125			
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp
	130					135					140				
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg
145					150					155					160
Asn	Asp	Thr	Phe	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu
				165					170					175	
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln
			180					185					190		
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu
		195					200					205			
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr
	210					215					220				
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala
225					230					235					240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg
			245						250					255	
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg
			260					265					270		
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr
		275					280					285			

Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	290	295	300	
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly	305	310	315	320
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	325	330	335	
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	340	345	350	
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	355	360	365	
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	370	375	380	
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	385	390	395	400
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	405	410	415	
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	420	425	430	
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	435	440	445	
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	450	455	460	
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	465	470	475	480
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	485	490	495	
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	500	505	510	
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	515	520	525	
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	530	535	540	
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	545	550	555	560
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr	565	570	575	
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp	580	585	590	

Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu
		595					600					605			
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro
	610					615					620				
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly
625					630					635					640
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro
				645					650					655	
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys
			660					665					670		

Ala

<210> 7
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1 Glu-164

<220>
 <221> CDS
 <222> (1)..(2019)

<400> 7																
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Met	Asn	Arg	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Pro	His	
1				5					10					15		
tgt	ggg	tgt	cca	tca	gat	gac	gat	gtg	agg	tat	cct	ttg	gca	agt	gac	96
Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
			20					25					30			
cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
		35					40					45				
aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
	50					55					60					
agt	ggg	aga	gat	gca	gtt	cag	act	gcg	ctt	act	gtt	gtt	ggg	aga	ata	240
Ser	Gly	Arg	Asp	Ala	Val	Gln	Thr	Ala	Leu	Thr	Val	Val	Gly	Arg	Ile	
65					70				75						80	
ctc	ggg	gct	tta	ggg	gtt	ccg	ttt	tct	gga	caa	ata	gtg	agt	ttt	tat	288
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Val	Ser	Phe	Tyr	
				85					90					95		

caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct ata tgg	336
Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp	
100 105 110	
gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa ata aca	384
Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr	
115 120 125	
gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gac	432
Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp	
130 135 140	
tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct gat cga	480
Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg	
145 150 155 160	
aat gat aca gaa aat tta agt gtt gtt cgt gct caa ttt ata gct tta	528
Asn Asp Thr Glu Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu	
165 170 175	
gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat gga cag	576
Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln	
180 185 190	
cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta cat ttg	624
Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu	
195 200 205	
tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga ttc aca	672
Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	
aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta gat cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg	
245 250 255	
tta aga gga aca aat act gaa agt tgg tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr	
275 280 285	
tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag gta tat aca gat ccg att gta ttt aat cca cca gct aat gtt gga	960
Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly	
305 310 315 320	
ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct gag ctc	1008

Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325					330					335		
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gat	agg	ctg	aat	agc	1056
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser	
			340					345					350			
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gat	1104
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp	
			355				360					365				
tat	tgg	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	
	370					375					380					
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
					390					395					400	
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	
				405					410					415		
ttt	cgt	tct	gca	ttg	ata	ggc	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	
			420					425					430			
gtc	cca	gga	ggc	ttg	ttt	aat	ggc	acg	act	tct	cct	gct	aat	gga	gga	1344
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
			435				440					445				
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	
			450			455					460					
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	gtt	acc	ttt	ttt	agc	ttt	1440
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe	
					470					475					480	
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	gta	cct	act	1488
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	
				485					490					495		
tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	acc	cca	1536
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
			500					505					510			
aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	gtt	tcg	1584
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	
			515				520					525				
ggc	act	acg	gtc	tta	aaa	ggc	cca	gga	ttt	aca	gga	ggg	ggc	ata	ctc	1632
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	
			530			535					540					
cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	gtt	aat	1680
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	

545		550		555		560	
tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc tca aca							1728
Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr							
		565		570		575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat							1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp							
		580		585		590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa							1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu							
		595		600		605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct							1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro							
		610		615		620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt							1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly							
		625		630		635	640
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct							1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro							
		645		650		655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa							2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys							
		660		665		670	
gcg							2019
Ala							

<210> 8
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 <212> PRT
 <213> Artificial sequence
 <223> Artificial sequence description: Cry9Ca1 Glu-164

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 Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp
 20 25 30
 Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met
 35 40 45
 Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile
 50 55 60
 Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile
 65 70 75 80
 Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr

85							90					95			
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp
		100					105						110		
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr
		115					120					125			
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Asp
		130				135					140				
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg
145					150					155					160
Asn	Asp	Thr	Glu	Asn	Leu	Ser	Val	Val	Arg	Ala	Gln	Phe	Ile	Ala	Leu
				165					170					175	
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln
			180					185					190		
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Val	Asn	Leu	His	Leu
		195					200					205			
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr
	210					215					220				
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Asp	Arg	Gln	Leu	Glu	Leu	Thr	Ala
225					230					235					240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Arg
			245					250					255		
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Trp	Leu	Arg	Tyr	His	Gln	Phe	Arg
			260					265					270		
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr
		275					280					285			
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg
	290					295					300				
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Val	Gly
305					310					315					320
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu
				325					330				335		
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Asp	Arg	Leu	Asn	Ser
			340					345					350		
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Asp
		355				360						365			
Tyr	Trp	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala
	370					375					380				
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile

385					390					395					400
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp
				405					410					415	
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe
			420					425					430		
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly
		435					440					445			
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser
	450					455					460				
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Val	Thr	Phe	Phe	Ser	Phe
465					470					475					480
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr
				485					490					495	
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro
			500					505					510		
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser
		515					520					525			
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu
	530					535					540				
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn
545					550					555					560
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala	Ser	Thr
				565					570					575	
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp
			580					585					590		
Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu
		595					600					605			
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro
	610					615					620				
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly
625					630					635					640
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro
				645					650					655	
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys
			660					665					670		

Ala

<210> 9
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1-100%

<220>
 <221> CDS
 <222> (1)..(2019)

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 tgt ggg tgt cca tca gaa gaa gaa tta agg tat cct ttg gca agt gaa 96
 Cys Gly Cys Pro Ser Glu Glu Glu Leu Arg Tyr Pro Leu Ala Ser Glu
 20 25 30
 cca aat gca gcg tta caa aat atg aac tat aaa gaa tac tta caa atg 144
 Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Glu Tyr Leu Gln Met
 35 40 45
 aca gaa gag gaa tac act gaa tct tat ata aat cct agt tta tct att 192
 Thr Glu Glu Glu Tyr Thr Glu Ser Tyr Ile Asn Pro Ser Leu Ser Ile
 50 55 60
 agt ggt aga gaa gca tta cag act gcg ctt act gtt att agg aga ata 240
 Ser Gly Arg Glu Ala Leu Gln Thr Ala Leu Thr Val Ile Arg Arg Ile
 65 70 75 80
 ctc ggg gct tta ggt tta ccg ttt tct gga caa ata tta agt ttt tat 288
 Leu Gly Ala Leu Gly Leu Pro Phe Ser Gly Gln Ile Leu Ser Phe Tyr
 85 90 95
 caa ttc ctt tta aat aca ctg ttt cca tta aat gaa aca gct ata ttt 336
 Gln Phe Leu Leu Asn Thr Leu Phe Pro Leu Asn Glu Thr Ala Ile Phe
 100 105 110
 gaa gct ttc atg cga cag tta gag gaa ctt tta aat caa caa ata aca 384
 Glu Ala Phe Met Arg Gln Leu Glu Glu Leu Leu Asn Gln Gln Ile Thr
 115 120 125
 gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta gga gaa 432
 Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Glu
 130 135 140
 tct ttt aat tta tat caa cgt tcc ctt caa aat ttt ttg gct gaa cga 480
 Ser Phe Asn Leu Tyr Gln Arg Ser Leu Gln Asn Phe Leu Ala Glu Arg
 145 150 155 160
 aat gaa aca cga aat tta agt tta tta cgt gct caa ttt ata gct tta 528
 Asn Glu Thr Arg Asn Leu Ser Leu Leu Arg Ala Gln Phe Ile Ala Leu
 165 170 175

gaa ctt gaa ttt tta aat gct att cca ttg ttt gca tta aat gga cag	576
Glu Leu Glu Phe Leu Asn Ala Ile Pro Leu Phe Ala Leu Asn Gly Gln	
180 185 190	
cag tta cca tta ctg tca tta tat gca caa gct tta aat tta cat ttg	624
Gln Leu Pro Leu Leu Ser Leu Tyr Ala Gln Ala Leu Asn Leu His Leu	
195 200 205	
tta tta tta aaa gaa gca tct ctt ttt gga gaa gga ttt gga ttc aca	672
Leu Leu Leu Lys Glu Ala Ser Leu Phe Gly Glu Gly Phe Gly Phe Thr	
210 215 220	
cag ggg gaa att tcc aca tat tat gaa cgt caa ttg gaa cta acc gct	720
Gln Gly Glu Ile Ser Thr Tyr Tyr Glu Arg Gln Leu Glu Leu Thr Ala	
225 230 235 240	
aag tac act aat tac tgt gaa act ttt tat aat aca ggt tta gaa cgt	768
Lys Tyr Thr Asn Tyr Cys Glu Thr Phe Tyr Asn Thr Gly Leu Glu Arg	
245 250 255	
tta aga gga aca aat act gaa agt ttt tta aga tat cat caa ttc cgt	816
Leu Arg Gly Thr Asn Thr Glu Ser Phe Leu Arg Tyr His Gln Phe Arg	
260 265 270	
aga gaa atg act tta tta tta tta gaa tta tta gcg cta ttt cca tat	864
Arg Glu Met Thr Leu Leu Leu Leu Glu Leu Leu Ala Leu Phe Pro Tyr	
275 280 285	
tat gaa tta cga ctt tat cca acg gga tca aac cca cag ctt aca cgt	912
Tyr Glu Leu Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg	
290 295 300	
gag tta tat aca gaa ccg att tta ttt aat cca cca gct aat tta gga	960
Glu Leu Tyr Thr Glu Pro Ile Leu Phe Asn Pro Pro Ala Asn Leu Gly	
305 310 315 320	
ctt tgc cga cgt ttt ggt act aat ccc tat aat act ttt tct gag ctc	1008
Leu Cys Arg Arg Phe Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu	
325 330 335	
gaa aat gcc ttc att cgc cca cca cat ctt ttt gaa agg ctg aat agc	1056
Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Glu Arg Leu Asn Ser	
340 345 350	
tta aca atc agc agt aat cga ttt cca tta tca tct aat ttt atg gaa	1104
Leu Thr Ile Ser Ser Asn Arg Phe Pro Leu Ser Ser Asn Phe Met Glu	
355 360 365	
tat ttt tca gga cat acg tta cgc cgt agt tat ctg aac gaa tca gca	1152
Tyr Phe Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Glu Ser Ala	
370 375 380	
tta caa gaa gaa agt tat ggc cta att aca acc aca aga gca aca att	1200
Leu Gln Glu Glu Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile	
385 390 395 400	

aat	ccc	gga	tta	gaa	gga	aca	aac	cgc	ata	gag	tca	acg	gca	tta	gaa	1248
Asn	Pro	Gly	Leu	Glu	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Leu	Glu	
				405					410					415		
ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	tta	aat	aga	gct	tct	ttt	1296
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Leu	Asn	Arg	Ala	Ser	Phe	
			420					425					430			
tta	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	gga	gga	1344
Leu	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
		435					440					445				
tgt	aga	gaa	ctc	tat	gaa	aca	aat	gaa	gaa	tta	cca	cca	gaa	gaa	agt	1392
Cys	Arg	Glu	Leu	Tyr	Glu	Thr	Asn	Glu	Glu	Leu	Pro	Pro	Glu	Glu	Ser	
	450					455					460					
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	tta	acc	ttt	ttt	agc	ttt	1440
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe	
465					470					475					480	
caa	act	aat	cag	gct	gga	tct	ata	gct	aat	gca	gga	agt	tta	cct	act	1488
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Leu	Pro	Thr	
			485					490						495		
tat	tta	ttt	acc	cgt	cgt	gaa	tta	gaa	ctt	aat	aat	acg	att	acc	cca	1536
Tyr	Leu	Phe	Thr	Arg	Arg	Glu	Leu	Glu	Leu	Asn	Asn	Thr	Ile	Thr	Pro	
			500					505					510			
aat	aga	att	aca	caa	tta	cca	ttg	tta	aag	gca	tct	gca	cct	tta	tcg	1584
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Leu	Lys	Ala	Ser	Ala	Pro	Leu	Ser	
		515				520						525				
ggg	act	acg	tta	tta	aaa	ggg	cca	gga	ttt	aca	gga	ggg	ggg	ata	ctc	1632
Gly	Thr	Thr	Leu	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	
	530					535					540					
cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	tta	acg	tta	aat	1680
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Leu	Thr	Leu	Asn	
545					550					555					560	
tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	tta	cgt	ttt	gcc	tca	aca	1728
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Leu	Arg	Phe	Ala	Ser	Thr	
				565				570					575			
gga	aat	ttc	agt	ata	agg	tta	ctc	cgt	gga	ggg	tta	tct	atc	ggg	gaa	1776
Gly	Asn	Phe	Ser	Ile	Arg	Leu	Leu	Arg	Gly	Gly	Leu	Ser	Ile	Gly	Glu	
			580					585					590			
tta	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	tac	gaa	1824
Leu	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu	
		595					600					605				
tcc	ttt	ttc	aca	aga	gag	ttt	act	act	act	ggg	ccg	ttc	aat	ccg	cct	1872
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro	
	610					615					620					
ttt	aca	ttt	aca	caa	gct	caa	gag	att	cta	aca	tta	aat	gca	gaa	ggg	1920

Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Leu	Asn	Ala	Glu	Gly		
625					630					635					640		
tta	agc	acc	ggt	ggt	gaa	tat	tat	ata	gaa	aga	att	gaa	att	tta	cct	1968	
Leu	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Glu	Arg	Ile	Glu	Ile	Leu	Pro		
			645						650					655			
tta	aat	ccg	gca	cga	gaa	gcg	gaa	gag	gaa	tta	gaa	gcg	gcg	aag	aaa	2016	
Leu	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Glu	Leu	Glu	Ala	Ala	Lys	Lys		
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gcg																2019	
Ala																	

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 <212> PRT
 <213> Artificial sequence
 <223> Artificial sequence description: Cry9Ca1-100%

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Cys	Gly	Cys	Pro	Ser	Glu	Glu	Glu	Leu	Arg	Tyr	Pro	Leu	Ala	Ser	Glu		
			20					25					30				
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Glu	Tyr	Leu	Gln	Met		
		35					40					45					
Thr	Glu	Glu	Glu	Tyr	Thr	Glu	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile		
		50				55					60						
Ser	Gly	Arg	Glu	Ala	Leu	Gln	Thr	Ala	Leu	Thr	Val	Ile	Arg	Arg	Ile		
	65				70					75					80		
Leu	Gly	Ala	Leu	Gly	Leu	Pro	Phe	Ser	Gly	Gln	Ile	Leu	Ser	Phe	Tyr		
				85					90					95			
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Phe	Pro	Leu	Asn	Glu	Thr	Ala	Ile	Phe		
		100						105					110				
Glu	Ala	Phe	Met	Arg	Gln	Leu	Glu	Glu	Leu	Leu	Asn	Gln	Gln	Ile	Thr		
		115					120					125					
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Glu		
	130					135					140						
Ser	Phe	Asn	Leu	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Phe	Leu	Ala	Glu	Arg		
145					150					155				160			
Asn	Glu	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu		
			165						170					175			
Glu	Leu	Glu	Phe	Leu	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Leu	Asn	Gly	Gln		
		180						185					190				

Gln	Leu	Pro	Leu	Leu	Ser	Leu	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu	
		195					200					205				
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Phe	Gly	Phe	Thr	
	210					215					220					
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
225					230					235					240	
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Phe	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	
			245						250					255		
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg	
			260					265					270			
Arg	Glu	Met	Thr	Leu	Leu	Leu	Leu	Glu	Leu	Leu	Ala	Leu	Phe	Pro	Tyr	
		275					280					285				
Tyr	Glu	Leu	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	
	290					295					300					
Glu	Leu	Tyr	Thr	Glu	Pro	Ile	Leu	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly	
305					310					315					320	
Leu	Cys	Arg	Arg	Phe	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	
				325					330					335		
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser	
			340					345					350			
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Leu	Ser	Ser	Asn	Phe	Met	Glu	
		355					360					365				
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Glu	Ser	Ala	
	370					375					380					
Leu	Gln	Glu	Glu	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	
385					390					395					400	
Asn	Pro	Gly	Leu	Glu	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Leu	Glu	
				405					410					415		
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Leu	Asn	Arg	Ala	Ser	Phe	
			420					425					430			
Leu	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	
		435					440					445				
Cys	Arg	Glu	Leu	Tyr	Glu	Thr	Asn	Glu	Glu	Leu	Pro	Pro	Glu	Glu	Ser	
	450					455					460					
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe	
465					470					475					480	
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Leu	Pro	Thr	
			485						490					495		

Tyr	Leu	Phe	Thr	Arg	Arg	Glu	Leu	Glu	Leu	Asn	Asn	Thr	Ile	Thr	Pro
			500					505					510		
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Leu	Lys	Ala	Ser	Ala	Pro	Leu	Ser
		515					520					525			
Gly	Thr	Thr	Leu	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu
	530					535					540				
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Leu	Thr	Leu	Asn
545					550					555					560
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Leu	Arg	Phe	Ala	Ser	Thr
				565					570					575	
Gly	Asn	Phe	Ser	Ile	Arg	Leu	Leu	Arg	Gly	Gly	Leu	Ser	Ile	Gly	Glu
			580					585					590		
Leu	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu
	595						600					605			
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro
	610					615					620				
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Leu	Asn	Ala	Glu	Gly
625					630				635						640
Leu	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Glu	Arg	Ile	Glu	Ile	Leu	Pro
			645						650					655	
Leu	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Glu	Leu	Glu	Ala	Ala	Lys	Lys
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Ala

<210> 11
 <211> 2019
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: Cry9Ca1-25%

<220>
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1				5					10				15			
tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca agt gac																96

Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp	
			20					25					30			
cca	aat	gca	gcg	tta	caa	aat	atg	aac	tat	aaa	gat	tac	tta	caa	atg	144
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met	
		35					40					45				
aca	gat	gag	gac	tac	act	gat	tct	tat	ata	aat	cct	agt	tta	tct	att	192
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile	
	50					55					60					
agt	ggt	aga	gaa	gca	tta	cag	act	gcg	ctt	acg	tta	tta	ggg	aga	ata	240
Ser	Gly	Arg	Glu	Ala	Leu	Gln	Thr	Ala	Leu	Thr	Leu	Leu	Gly	Arg	Ile	
65					70					75					80	
ctc	ggg	gct	tta	ggt	gtt	ccg	ttt	tct	gga	caa	ata	tta	agt	ttt	tat	288
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Leu	Ser	Phe	Tyr	
				85					90					95		
caa	ttc	ctt	tta	aat	aca	ctg	tgg	cca	gtt	aat	gat	aca	gct	ata	tgg	336
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp	
			100					105					110			
gaa	gct	ttc	atg	cga	cag	gtg	gag	gaa	ctt	gtc	aat	caa	caa	ata	aca	384
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr	
		115					120					125				
gaa	ttt	gca	aga	aat	cag	gca	ctt	gca	aga	ttg	caa	gga	tta	gga	gaa	432
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Glu	
	130					135					140					
tct	ttt	aat	gta	tat	caa	cgt	tcc	ctt	caa	aat	tgg	ttg	gct	gat	cga	480
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg	
145					150					155					160	
aat	gat	aca	cga	aat	tta	agt	tta	tta	cgt	gct	caa	ttt	ata	gct	tta	528
Asn	Asp	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu	
				165					170					175		
gac	ctt	gat	ttt	gtt	aat	gct	att	cca	ttg	ttt	gca	gta	aat	gga	cag	576
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln	
			180					185					190			
cag	gtt	cca	tta	ctg	tca	gta	tat	gca	caa	gct	tta	aat	tta	cat	ttg	624
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu	
		195					200					205				
tta	tta	tta	aaa	gaa	gca	tct	ctt	ttt	gga	gaa	gga	tgg	gga	ttc	aca	672
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr	
	210					215					220					
cag	ggg	gaa	att	tcc	aca	tat	tat	gaa	cgt	caa	ttg	gaa	cta	acc	gct	720
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala	
225					230					235					240	
aag	tac	act	aat	tac	tgt	gaa	act	tgg	tat	aat	aca	ggt	tta	gaa	cgt	768
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	

245								250					255					
tta	aga	gga	aca	aat	act	gaa	agt	ttt	tta	aga	tat	cat	caa	ttc	cgt	816		
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg			
			260					265					270					
aga	gaa	atg	act	tta	gtg	gta	tta	gat	gtt	gtg	gcg	cta	ttt	cca	tat	864		
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr			
		275					280					285						
tat	gat	gta	cga	ctt	tat	cca	acg	gga	tca	aac	cca	cag	ctt	aca	cgt	912		
Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg			
	290					295					300							
gag	gta	tat	aca	gat	ccg	att	gta	ttt	aat	cca	cca	gct	aat	tta	gga	960		
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly			
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ctt	tgc	cga	cgt	tgg	ggg	act	aat	ccc	tat	aat	act	ttt	tct	gag	ctc	1008		
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu			
				325				330					335					
gaa	aat	gcc	ttc	att	cgc	cca	cca	cat	ctt	ttt	gaa	agg	ctg	aat	agc	1056		
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser			
			340					345					350					
tta	aca	atc	agc	agt	aat	cga	ttt	cca	gtt	tca	tct	aat	ttt	atg	gaa	1104		
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Glu			
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tat	ttt	tca	gga	cat	acg	tta	cgc	cgt	agt	tat	ctg	aac	gat	tca	gca	1152		
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala			
	370					375					380							
gta	caa	gaa	gat	agt	tat	ggc	cta	att	aca	acc	aca	aga	gca	aca	att	1200		
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile			
385					390					395				400				
aat	ccc	gga	gtt	gat	gga	aca	aac	cgc	ata	gag	tca	acg	gca	gta	gat	1248		
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp			
				405				410					415					
ttt	cgt	tct	gca	ttg	ata	ggg	ata	tat	ggc	gtg	aat	aga	gct	tct	ttt	1296		
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe			
			420				425					430						
gtc	cca	gga	ggc	ttg	ttt	aat	ggg	acg	act	tct	cct	gct	aat	gga	gga	1344		
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly			
		435				440					445							
tgt	aga	gat	ctc	tat	gat	aca	aat	gat	gaa	tta	cca	cca	gat	gaa	agt	1392		
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser			
	450					455					460							
acc	gga	agt	tca	acc	cat	aga	cta	tct	cat	tta	acc	ttt	ttt	agc	ttt	1440		
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe			
465					470					475				480				

caa act aat cag gct gga tct ata gct aat gca gga agt gta cct act	1488
Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr	
485 490 495	
tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att acc cca	1536
Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro	
500 505 510	
aat aga att aca caa tta cca ttg gta aag gca tct gca cct gtt tcg	1584
Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser	
515 520 525	
ggg act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt ata ctc	1632
Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu	
530 535 540	
cga aga aca act aat ggc aca ttt gga acg tta aga gta acg gtt aat	1680
Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn	
545 550 555 560	
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Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Leu Arg Phe Ala Ser Thr	
565 570 575	
gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc ggt gat	1776
Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp	
580 585 590	
gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act tac gaa	1824
Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu	
595 600 605	
tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat ccg cct	1872
Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro	
610 615 620	
ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca gaa ggt	1920
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly	
625 630 635 640	
gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att gtc cct	1968
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro	
645 650 655	
gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg aag aaa	2016
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys	
660 665 670	
gcg	2019
Ala	

<210> 12

<211> 673

<212> PRT

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<223> Artificial sequence description: Cry9Ca1-25%

<400> 12

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1				5					10					15	
Cys	Gly	Cys	Pro	Ser	Asp	Asp	Asp	Val	Arg	Tyr	Pro	Leu	Ala	Ser	Asp
			20					25					30		
Pro	Asn	Ala	Ala	Leu	Gln	Asn	Met	Asn	Tyr	Lys	Asp	Tyr	Leu	Gln	Met
		35					40					45			
Thr	Asp	Glu	Asp	Tyr	Thr	Asp	Ser	Tyr	Ile	Asn	Pro	Ser	Leu	Ser	Ile
	50					55					60				
Ser	Gly	Arg	Glu	Ala	Leu	Gln	Thr	Ala	Leu	Thr	Leu	Leu	Gly	Arg	Ile
65					70					75					80
Leu	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ser	Gly	Gln	Ile	Leu	Ser	Phe	Tyr
				85					90					95	
Gln	Phe	Leu	Leu	Asn	Thr	Leu	Trp	Pro	Val	Asn	Asp	Thr	Ala	Ile	Trp
			100					105					110		
Glu	Ala	Phe	Met	Arg	Gln	Val	Glu	Glu	Leu	Val	Asn	Gln	Gln	Ile	Thr
		115					120					125			
Glu	Phe	Ala	Arg	Asn	Gln	Ala	Leu	Ala	Arg	Leu	Gln	Gly	Leu	Gly	Glu
	130					135					140				
Ser	Phe	Asn	Val	Tyr	Gln	Arg	Ser	Leu	Gln	Asn	Trp	Leu	Ala	Asp	Arg
145					150					155					160
Asn	Asp	Thr	Arg	Asn	Leu	Ser	Leu	Leu	Arg	Ala	Gln	Phe	Ile	Ala	Leu
				165					170					175	
Asp	Leu	Asp	Phe	Val	Asn	Ala	Ile	Pro	Leu	Phe	Ala	Val	Asn	Gly	Gln
			180					185					190		
Gln	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Leu	Asn	Leu	His	Leu
		195					200					205			
Leu	Leu	Leu	Lys	Glu	Ala	Ser	Leu	Phe	Gly	Glu	Gly	Trp	Gly	Phe	Thr
	210					215					220				
Gln	Gly	Glu	Ile	Ser	Thr	Tyr	Tyr	Glu	Arg	Gln	Leu	Glu	Leu	Thr	Ala
225					230					235					240
Lys	Tyr	Thr	Asn	Tyr	Cys	Glu	Thr	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg
			245						250					255	
Leu	Arg	Gly	Thr	Asn	Thr	Glu	Ser	Phe	Leu	Arg	Tyr	His	Gln	Phe	Arg
			260					265					270		
Arg	Glu	Met	Thr	Leu	Val	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Tyr
		275					280					285			

Tyr	Asp	Val	Arg	Leu	Tyr	Pro	Thr	Gly	Ser	Asn	Pro	Gln	Leu	Thr	Arg	290	295	300	
Glu	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Pro	Pro	Ala	Asn	Leu	Gly	305	310	315	320
Leu	Cys	Arg	Arg	Trp	Gly	Thr	Asn	Pro	Tyr	Asn	Thr	Phe	Ser	Glu	Leu	325	330	335	
Glu	Asn	Ala	Phe	Ile	Arg	Pro	Pro	His	Leu	Phe	Glu	Arg	Leu	Asn	Ser	340	345	350	
Leu	Thr	Ile	Ser	Ser	Asn	Arg	Phe	Pro	Val	Ser	Ser	Asn	Phe	Met	Glu	355	360	365	
Tyr	Phe	Ser	Gly	His	Thr	Leu	Arg	Arg	Ser	Tyr	Leu	Asn	Asp	Ser	Ala	370	375	380	
Val	Gln	Glu	Asp	Ser	Tyr	Gly	Leu	Ile	Thr	Thr	Thr	Arg	Ala	Thr	Ile	385	390	395	400
Asn	Pro	Gly	Val	Asp	Gly	Thr	Asn	Arg	Ile	Glu	Ser	Thr	Ala	Val	Asp	405	410	415	
Phe	Arg	Ser	Ala	Leu	Ile	Gly	Ile	Tyr	Gly	Val	Asn	Arg	Ala	Ser	Phe	420	425	430	
Val	Pro	Gly	Gly	Leu	Phe	Asn	Gly	Thr	Thr	Ser	Pro	Ala	Asn	Gly	Gly	435	440	445	
Cys	Arg	Asp	Leu	Tyr	Asp	Thr	Asn	Asp	Glu	Leu	Pro	Pro	Asp	Glu	Ser	450	455	460	
Thr	Gly	Ser	Ser	Thr	His	Arg	Leu	Ser	His	Leu	Thr	Phe	Phe	Ser	Phe	465	470	475	480
Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val	Pro	Thr	485	490	495	
Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile	Thr	Pro	500	505	510	
Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro	Val	Ser	515	520	525	
Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly	Ile	Leu	530	535	540	
Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr	Val	Asn	545	550	555	560
Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Leu	Arg	Phe	Ala	Ser	Thr	565	570	575	
Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile	Gly	Asp	580	585	590	

Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr	Tyr	Glu
		595					600					605			
Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn	Pro	Pro
	610					615					620				
Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala	Glu	Gly
625					630					635					640
Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile	Val	Pro
				645					650					655	
Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala	Lys	Lys
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<210> 14
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<400> 14
 gaattaaatg aattattaaa tttaagtgtt 30

<210> 15
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<400> 15
 gaattattag aattttttatt attaagtgtt 30

<210> 16

<211> 30
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 <220>
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 <400> 16
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 <210> 17
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 <220>
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 <400> 17
 gaattattag aagaattatt attaagtggt 30

 <210> 18
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 <400> 18
 gaacgattag aattttttatt attaagtggt 30

 <210> 19
 <211> 30
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 <220>
 <223> Artificial sequence description: mutant 7

 <400> 19
 gaacgattag aattattatt attaagtggt 30

 <210> 20
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 <220>
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 <400> 20
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<210> 21
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<220>
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<400> 21
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<210> 22
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tttttattaa atttatTTTT tttaccatta ctg 33

<210> 23
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<210> 24
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<210> 25
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tttgaagaaa atttttttatt atttccatta ctg 33

<210> 26
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tttgaagaaa attttgaaga atttccatta ctg 33

<210> 27
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tttttattaa attttgaaga atttccatta ctg 33

<210> 28
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tttttattaa atgaattttt tgaaccatta ctg 33

<210> 29
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<220>
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<400> 29
cttttttttag aattattttt attc 24

<210> 30
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<220>
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<400> 30
cttttttttat tattattttt attc

24

<210> 31
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<223> Artificial sequence description: mutant 19

<400> 31
cttttttttag aagaatttga atta

24

<210> 32
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<223> Artificial sequence description: mutant 20

<400> 32
cttttttgaag aagaatttga atta

24

<210> 33
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<220>
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cttttttgaag aattatttga agaa

24

<210> 34
<211> 15
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<220>
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<400> 34
ttattagaat taaat

15

<210> 35

<211> 15
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<400> 35
ttattatttt taaat 15

<210> 36
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<400> 36
ttagaattat taaat 15

<210> 37
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<400> 37
ttattatttt ttaat 15

<210> 38
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<400> 38
ttagaagaat taaat 15

<210> 39
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<400> 39
ttagaatttt taaat 15

<210> 40
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<400> 40
ttagaatttg aaaat 15

<210> 41
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<220>
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<400> 41
ttagaagaag aaaat 15

<210> 42
<211> 33
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<400> 42
gatcgaaatg atacattaaa tttaagtgtt gtt 33

<210> 43
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<220>
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oligonucleotide 2

<400> 43
gatcgaaatg atacatttaa tttaagtgtt gtt 33

<210> 44
<211> 33
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<223> Artificial sequence description:
oligonucleotide 3

<400> 44

gatcgaaatg atacagaaaa tttaagtgtt gtt

33

<210> 45

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 4

<400> 45

cgaaatgata cacgattatt aagtgttggtt cgt

33

<210> 46

<211> 33

<212> DNA

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<220>

<223> Artificial sequence description:
oligonucleotide 5

<400> 46

cgaaatgata cacgagaatt aagtgttggtt cgt

33

<210> 47

<211> 39

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<223> Artificial sequence description:
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<400> 47

ttggctgata gaaatgaatt tttaaattta agtgttggtt

39

<210> 48

<211> 39

<212> DNA

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<223> Artificial sequence description:
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<400> 48

ttggctgatc gaaatgaatt tttattatta agtggtggt 39

<210> 49
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<400> 49
ttggctgatc gaaatgaatt attaaattta agtggtggt 39

<210> 50
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<400> 50
ttggctgatc gaaatgaatt attattatta agtggtggt 39

<210> 51
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<400> 51
ttggctgatc gaaatgaaga agaagaatta agtggtggt 39

<210> 52
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<400> 52
ttggctgatc gaaatgaaga attattatta agtggtggt 39

<210> 53
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<400> 53
caaaattggt tggctgaatt aaatgaatta ttaaat 36

<210> 54
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oligonucleotide 13

<400> 54
caaaattggt tggctgaatt aaatgaattt ttaaat 36

<210> 55
<211> 39
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oligonucleotide 14

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caaaattggt tggctgaatt attagaattt ttattatta 39

<210> 56
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oligonucleotide 15

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caaaattggt tggctgaatt attagaatta ttattatta 39

<210> 57
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oligonucleotide 16

<400> 57

caaaattggt tggctgaatt attagaagaa ttattatta

39

<210> 58

<211> 39

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<223> Artificial sequence description:
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<400> 58

caaaattggt tggctgaacg attagaattt ttattatta

39

<210> 59

<211> 39

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<400> 59

caaaattggt tggctgaacg attagaatta ttattatta

39

<210> 60

<211> 39

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caaaattggt tggctgaatt agaagaatta ttattatta

39

<210> 61

<211> 39

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<223> Artificial sequence description:
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<400> 61

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39

<210> 62
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<210> 63
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<210> 64
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ttattaaatg gacagcagtt accattactg tcagta 36

<210> 65
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<400> 65
ttattaaatg gacagcagtt tccattactg tcagta 36

<210> 66
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<400> 66
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<210> 67
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<400> 67
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<210> 68
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<210> 69
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<400> 69
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<210> 70
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<210> 71
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oligonucleotide 30

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<210> 72
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oligonucleotide 31

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<210> 73
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oligonucleotide 32

<400> 73
ccattgtttg aagaaaattt tgaagaattt ccattactgt cagta 45

<210> 74
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oligonucleotide 33

<400> 74
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<210> 75

<211> 45
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oligonucleotide 34

<400> 75
ccattgtttt tattaaatga attttttgaa ccattactgt cagta 45

<210> 76
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oligonucleotide 35

<400> 76
gatgcatctc tttttttaga aggatgggga ttc 33

<210> 77
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oligonucleotide 36

<400> 77.
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<210> 78
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<400> 78
gatgcatctc tttttgaaga aggatgggga ttc 33

<210> 79
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<223> Artificial sequence description:
oligonucleotide 38

<400> 79

ttagaaggat ggggattaac acagggggaa att

33

<210> 80

<211> 33

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<223> Artificial sequence description:
oligonucleotide 39

<400> 80

gaagaaggat ggggagaaac acagggggaa att

33

<210> 81

<211> 45

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oligonucleotide 40

<400> 81

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45

<210> 82

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oligonucleotide 41

<400> 82

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<210> 83

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<400> 83

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<210> 84
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oligonucleotide 43

<400> 84
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<210> 85
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oligonucleotide 44

<400> 85
gcatctcttt ttgaagaatt atttttagaa acacaggggg aaatt 45

<210> 86
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oligonucleotide 45

<400> 86
ggtttagatc gtttattaga attaaatact gaaagttgg 39

<210> 87
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oligonucleotide 46

<400> 87
ggtttagatc gtttattatt tttaaatact gaaagttgg 39

<210> 88
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<223> Artificial sequence description:
oligonucleotide 47

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ggtttagatc gtttagaatt attaaatact gaaagttgg

39

<210> 89

<211> 39

<212> DNA

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oligonucleotide 48

<400> 89

ggtttagatc gtttattatt ttttaatact gaaagttgg

39

<210> 90

<211> 39

<212> DNA

<213> Artificial sequence

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oligonucleotide 49

<400> 90

ggtttagatc gtttagaaga attaaatact gaaagttgg

39

<210> 91

<211> 39

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<213> Artificial sequence

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<223> Artificial sequence description:
oligonucleotide 50

<400> 91

ggtttagatc gtttagaatt tttaaatact gaaagttgg

39

<210> 92

<211> 39

<212> DNA

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<223> Artificial sequence description:
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ggtttagatc gtttagaatt tgaaaatact gaaagttgg 39

<210> 93
<211> 39
<212> DNA
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<223> Artificial sequence description:
oligonucleotide 52

<400> 93
ggtttagatc gtttagaaga agaaaatact gaaagttgg 39

<210> 94
<211> 30
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oligonucleotide 53

<400> 94
tgaatatgaa attattgaag cccccattg 30

<210> 95
<211> 40
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<223> Artificial sequence description:
oligonucleotide 54

<400> 95
tgggtgtcca tcagaagaag aattaaggta tcctttggca 40

<210> 96
<211> 27
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 55

<400> 96
tcctttggca agtgaaccaa atgcagc 27

<210> 97
<211> 25
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 56

<400> 97
gaactataaa gaatacttac aaatg

25

<210> 98
<211> 26
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<220>
<223> Artificial sequence description:
oligonucleotide 57

<400> 98
caaatgacag aagaggaata cactga

26

<210> 99
<211> 20
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<223> Artificial sequence description:
oligonucleotide 58

<400> 99
tacactgaat cttatataaa

20

<210> 100
<211> 36
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 59

<400> 100
tattagtggg agagaagcat tacagactgc gcttac

36

<210> 101
<211> 37
<212> DNA
<213> Artificial sequence

<220>
 <223> Artificial sequence description:
 oligonucleotide 60

<400> 101
 cagactgcgc ttactgttat tagggagaat actcggg 37

<210> 102
 <211> 25
 <212> DNA
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<220>
 <223> Artificial sequence description:
 oligonucleotide 61

<400> 102
 gggctttagg ttaccgttt tctgg 25

<210> 103
 <211> 28
 <212> DNA
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<220>
 <223> Artificial sequence description:
 oligonucleotide 62

<400> 103
 ttctggacaa atattaagtt tttatcaa 28

<210> 104
 <211> 40
 <212> DNA
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<220>
 <223> Artificial sequence description:
 oligonucleotide 63

<400> 104
 ctttttaaata cactgtttcc attaaatgaa acagctatat 40

<210> 105
 <211> 24
 <212> DNA
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<220>
 <223> Artificial sequence description:
 oligonucleotide 64

<400> 105

acagctatat ttgaagcttt catg 24

<210> 106
<211> 26
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 65

<400> 106
ctttcatgcg acagttagag gaactt 26

<210> 107
<211> 26
<212> DNA
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<223> Artificial sequence description:
oligonucleotide 66

<400> 107
gaggaacttt taaatcaaca aataac 26

<210> 108
<211> 21
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 67

<400> 108
ggattaggag aatcttttaa t 21

<210> 109
<211> 23
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 68

<400> 109
tcttttaatt tatatcaacg ttc 23

<210> 110
<211> 21

<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 69

<400> 110
ccttcaaaat tttttggctg a

21

<210> 111
<211> 17
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 70

<400> 111
ttggctgaac gaaatga

17

<210> 112
<211> 23
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 71

<400> 112
cgaaatgaaa cacgaaattt aag

23

<210> 113
<211> 37
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 72

<400> 113
acacgaaatt taagtttatt acgtgctcaa tttatag

37

<210> 114
<211> 48
<212> DNA
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<220>
<223> Artificial sequence description:

oligonucleotide 73

<400> 114
gctcaattta tagctttaga acttgaattt ttaaattgcta ttccattg 48

<210> 115
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 74

<400> 115
ccattgtttg cattaaatgg acagcag 27

<210> 116
<211> 27
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 75

<400> 116
ccattgtttg cattaaatgg acagcag 27

<210> 117
<211> 27
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oligonucleotide 76

<400> 117
ccattactgt cattatatgc acaagct 27

<210> 118
<211> 27
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oligonucleotide 77

<400> 118
tatgcacaag ctttaaattt acatttg 27

<210> 119
<211> 23
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 78

<400> 119
ttattaaaag aagcatctct ttt

23

<210> 120
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 79

<400> 120
tggagaagga tttggattca cacag

25

<210> 121
<211> 24
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 80

<400> 121
cacatattat gaacgtcaat tgga

24

<210> 122
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 81

<400> 122
tactgtgaaa ctttttataa tacagggtt

28

<210> 123
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 82

<400> 123
tacaggttta gaacgttta gagga

25

<210> 124
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 83

<400> 124
aatactgaaa gttttttaag atatcatc

28

<210> 125
<211> 51
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 84

<400> 125
gtagagaaat gactttatta ttattagaat tattagcgct atttccatat t

51

<210> 126
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 85

<400> 126
atattatgaa ttacgacttt atccaac

27

<210> 127
<211> 23
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 86

<400> 127
cttacacgtg agttatatac aga 23

<210> 128
<211> 29
<212> DNA
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<220>
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oligonucleotide 87

<400> 128
tatacagaac cgattttatt taatccacc 29

<210> 129
<211> 28
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oligonucleotide 88

<400> 129
ccaccagcta atttaggact ttgccgac 28

<210> 130
<211> 27
<212> DNA
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<220>
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oligonucleotide 89

<400> 130
ctttgccgac gttttggtac taatccc 27

<210> 131
<211> 23
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 90

<400> 131
catcttttttg aaaggctgaa tag 23

<210> 132

<211> 30
<212> DNA
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<220>
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oligonucleotide 91

<400> 132
taatcgattt ccattatcat ctaattttat

30

<210> 133
<211> 36
<212> DNA
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<220>
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oligonucleotide 92

<400> 133
ctaattttat ggaatatttt tcaggacata cgttac

36

<210> 134
<211> 33
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 93

<400> 134
tagttatctg aacgaatcag cattacaaga aga

33

<210> 135
<211> 20
<212> DNA
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<220>
<223> Artificial sequence description:
oligonucleotide 94

<400> 135
caagaagaaa gttatggcct

20

<210> 136
<211> 35
<212> DNA
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<220>

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<210> 141
<211> 17
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<213> Artificial sequence

<220>
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oligonucleotide 100

<400> 141
ctctatgaaa caaatga

17

<210> 142
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 101

<400> 142
acaaatgaag aattaccacc

20

<210> 143
<211> 27
<212> DNA
<213> Artificial sequence

<220>
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oligonucleotide 102

<400> 143
attaccacca gaagaaagta ccggaag

27

<210> 144
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description:
oligonucleotide 103

<400> 144
agactatctc atttaacctt ttttagcttt

30

<210> 145
<211> 27
<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 104

<400> 145

gctaatgcag gaagtttacc tacttat

27

<210> 146

<211> 26

<212> DNA

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<220>

<223> Artificial sequence description:
oligonucleotide 105

<400> 146

cctacttatt tat ttaccgcg tcgtga

26

<210> 147

<211> 33

<212> DNA

<213> Artificial sequence

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<223> Artificial sequence description:
oligonucleotide 106

<400> 147

accgcgtcgtg aattagaact taataatacg att

33

<210> 148

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description:
oligonucleotide 107

<400> 148

attaccattg ttaaaggcat ctgc

24

<210> 149

<211> 30

<212> DNA

<213> Artificial sequence

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<223> Artificial sequence description:
oligonucleotide 108

<p><400> 149 aaggcatctg cacctttatc gggactacg</p>	30
<p><210> 150 <211> 29 <212> DNA <213> Artificial sequence</p>	
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<p><400> 150 tcgggtacta cgttattaaa aggtccagg</p>	29
<p><210> 151 <211> 40 <212> DNA <213> Artificial sequence</p>	
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<p><400> 152 cacaacaata tcgcctaaga ttacgttttg cctcaac</p>	37
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<p><400> 153 aaatttcagt ataaggttac tccgtggagg g</p>	31

<210> 154
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oligonucleotide 113

<400> 154
ataagggtac tccgtggagg gttatctatc ggtga

35

<210> 155
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<220>
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oligonucleotide 114

<400> 155
tctatcggtg aattaagatt agggagcac

29

<210> 156
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oligonucleotide 115

<400> 156
caagagattc taacatta aa tgcagaaggt

30

<210> 157
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oligonucleotide 116

<400> 157
aatgcagaag gtttaagcac cggtggtgaa ta

32

<210> 158
<211> 32
<212> DNA
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oligonucleotide 117

<400> 158
gtggtgaata ttatatagaa agaattgaaa tt

32

<210> 159
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<212> DNA
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oligonucleotide 118

<400> 159
agaattgaaa ttttaccttt aaatccggca cgagaag

37

<210> 160
<211> 30
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<223> Artificial sequence description:
oligonucleotide 119

<400> 160
cgagaagcgg aagaggaatt agaagcggcg
1

30